

## SEQUENCE LISTING

<110> Short, Jay M.  
 Kretz, Keith A.  
 Gray, Kevin A.  
 Barton, Nelson Robert  
 Garrett, James B.  
 O' Donoghue, Eileen  
 Mathur, Eric J.

<120> RECOMBINANT PHYTASES AND METHODS OF MAKING AND USING THEM

<130> 09010-029006

<140>

<141> 2003-06-20

<150> US 09/866,379

<151> 2001-05-24

<150> US 09/580,515

<151> 2000-05-25

<150> US 09/318,528

<151> 1999-05-25

<150> US 09/291,931

<151> 1999-04-13

<150> US 09/259,214

<151> 1999-03-01

<150> US 08/910,798

<151> 1997-08-13

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<221> misc\_feature

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10306703.txt

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Gly	Arg	Ile	Thr	Asp	Ser	His	Gln	Trp	Asn	Thr	Leu	Leu	Ser	Leu	His		
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## 10306703.txt

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Trp	Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	Arg	Asp	
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 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr  
 35 40 45  
 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val  
 50 55 60  
 Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu  
 65 70 75 80  
 Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys  
 85 90 95  
 Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp  
 100 105 110  
 Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro  
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## 10306703.txt

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 Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu  
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 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala  
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 Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His  
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 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu  
 305 310 315 320  
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu  
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 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly  
 340 345 350  
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln  
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 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp  
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 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala  
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## 10306703.txt

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tgatgcggcg cattagcatc gcatcaggca atcaataatg tcagatatga aaagcggaaa 180
catatcg atg aaa gcg atc tta atc cca ttt tta tct ctt ctg att ccg 229
Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro
1 5 10

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tta acc ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg 277
Leu Thr Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu
15 20 25 30

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gaa agt gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag 325
Glu Ser Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys
35 40 45

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gcc acg caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg 373
Ala Thr Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp
50 55 60

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ccg gta aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc 421
Pro Val Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala
65 70 75

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tat ctc gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg 469
Page 6

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## 10306703.txt

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Ala	Lys	Lys	Gly	Cys	Pro	Gln	Ser	Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	
95					100				105						110	
gtc	gac	gag	cgt	acc	cgt	aaa	aca	ggc	gaa	gcc	ttc	gcc	gcc	ggg	ctg	565
Val	Asp	Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	
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gca	cct	gac	tgt	gca	ata	acc	gta	cat	acc	cag	gca	gat	acg	tcc	agt	613
Ala	Pro	Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	
			130					135					140			
ccc	gat	ccg	tta	ttt	aat	cct	cta	aaa	act	ggc	gtt	tgc	caa	ctg	gat	661
Pro	Asp	Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr	Gly	Val	Cys	Gln	Leu	Asp	
		145					150					155				
aac	gcg	aac	gtg	act	gac	gcg	atc	ctc	agc	agg	gca	gga	ggg	tca	att	709
Asn	Ala	Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser	Arg	Ala	Gly	Gly	Ser	Ile	
	160					165					170					
gct	gac	ttt	acc	ggg	cat	cgg	caa	acg	gcg	ttt	cgc	gaa	ctg	gaa	cgg	757
Ala	Asp	Phe	Thr	Gly	His	Arg	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	
175					180				185						190	
gtg	ctt	aat	ttt	ccg	caa	tca	aac	ttg	tgc	ctt	aaa	cgt	gag	aaa	cag	805
Val	Leu	Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	
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gac	gaa	agc	tgt	tca	tta	acg	cag	gca	tta	cca	tcg	gaa	ctc	aag	gtg	853
Asp	Glu	Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	
			210					215					220			
agc	gcc	gac	aat	gtc	tca	tta	acc	ggt	gcg	gta	agc	ctc	gca	tca	atg	901
Ser	Ala	Asp	Asn	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	
		225					230					235				
ctg	acg	gag	ata	ttt	ctc	ctg	caa	caa	gca	cag	gga	atg	ccg	gag	ccg	949
Leu	Thr	Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	
	240					245					250					
ggg	tgg	gga	agg	atc	acc	gat	tca	cac	cag	tgg	aac	acc	ttg	cta	agt	997
Gly	Trp	Gly	Arg	Ile	Thr	Asp	Ser	His	Gln	Trp	Asn	Thr	Leu	Leu	Ser	
255					260				265						270	
ttg	cat	aac	gcg	caa	ttt	tat	ttg	cta	caa	cgc	acg	cca	gag	gtt	gcc	1045
Leu	His	Asn	Ala	Gln	Phe	Tyr	Leu	Leu	Gln	Arg	Thr	Pro	Glu	Val	Ala	
				275					280					285		
cgc	agc	cgc	gcc	acc	ccg	tta	tta	gat	ttg	atc	aag	aca	gcg	ttg	acg	1093
Arg	Ser	Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu	Ile	Lys	Thr	Ala	Leu	Thr	
			290					295					300			
ccc	cat	cca	ccg	caa	aaa	cag	gcg	tat	ggt	gtg	aca	tta	ccc	act	tca	1141
Pro	His	Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly	Val	Thr	Leu	Pro	Thr	Ser	
		305					310					315				
gtg	ctg	ttt	atc	gcc	gga	cac	gat	act	aat	ctg	gca	aat	ctc	ggc	ggc	1189
Val	Leu	Phe	Ile	Ala	Gly	His	Asp	Thr	Asn	Leu	Ala	Asn	Leu	Gly	Gly	
	320					325					330					

## 10306703.txt

gca ctg gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg 1237  
 Ala Leu Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro  
 335 340 345 350

cca ggt ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac 1285  
 Pro Gly Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn  
 355 360 365

agc cag tgg att cag gtt tct ctg gtc ttc cag act tta cag cag atg 1333  
 Ser Gln Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met  
 370 375 380

cgt gat aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa 1381  
 Arg Asp Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys  
 385 390 395

ctg acc ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tct 1429  
 Leu Thr Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser  
 400 405 410

ttg gca ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc 1477  
 Leu Ala Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys  
 415 420 425 430

agt ttg taatgcataa aaaagagcat tcagttacct gaatgctctg aggctgatga 1533  
 Ser Leu

caaacgaaga actgtctaat gcgtagaccg gaaaaggcgt tcacgccgca tccggccact 1593  
 ttcagttttc ctctttctcg gagtaactat aaccgtaata gttatagccg taactgtaag 1653  
 cgggtgctggc gcgtttaatc acaccattga ggatagcgcc tttaatatgg acgcctgcct 1713  
 gttccagacg ctgcattgac aaactcacct ctttgccggt gttcaagcca aaacgcgcaa 1773  
 ccagcaggct ggtgccaaca gaacgccccca cgaccgcggc atcactcacc gccagcatcg 1833  
 gcggcgatc gacaatcacc agatcgtaaat ggctgcttcgc ccattccagt aattgacgca 1893  
 tccgatcg 1901

<210> 8

<211> 432

<212> PRT

<213> Escherichia coli

<400> 8

Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr  
 1 5 10 15  
 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser  
 20 25 30  
 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr  
 35 40 45  
 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val  
 50 55 60  
 Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu  
 65 70 75 80  
 Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys  
 85 90 95  
 Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp  
 100 105 110  
 Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro  
 115 120 125  
 Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp  
 130 135 140  
 Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala  
 145 150 155 160  
 Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp



## 10306703.txt

165  
 Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu  
 180 185 190  
 Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu  
 195 200 205  
 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala  
 210 215 220  
 Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr  
 225 230 235 240  
 Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp  
 245 250 255  
 Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His  
 260 265 270  
 Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser  
 275 280 285  
 Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His  
 290 295 300  
 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu  
 305 310 315 320  
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu  
 325 330 335  
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly  
 340 345 350  
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln  
 355 360 365  
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp  
 370 375 380  
 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr  
 385 390 395 400  
 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala  
 405 410 415  
 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu  
 420 425 430

&lt;210&gt; 9

&lt;211&gt; 1308

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; modified phytase enzyme

&lt;221&gt; CDS

&lt;222&gt; (1)...(1296)

&lt;400&gt; 9

atg	aaa	gcg	atc	tta	atc	cca	ttt	tta	tct	ctt	ctg	att	ccg	tta	acc	48
Met	Lys	Ala	Ile	Leu	Ile	Pro	Phe	Leu	Ser	Leu	Leu	Ile	Pro	Leu	Thr	
1				5				10						15		

ccg	caa	tct	gca	ttc	gct	cag	agt	gag	ccg	gag	ctg	aag	ctg	gaa	agt	96
Pro	Gln	Ser	Ala	Phe	Ala	Gln	Ser	Glu	Pro	Glu	Leu	Lys	Leu	Glu	Ser	
			20					25					30			

ccg	caa	tct	gca	ttc	gct	cag	agt	gag	ccg	gag	ctg	aag	ctg	gaa	agt	96
Pro	Gln	Ser	Ala	Phe	Ala	Gln	Ser	Glu	Pro	Glu	Leu	Lys	Leu	Glu	Ser	
			20					25					30			

gtg	gtg	att	gtc	agt	cgt	cat	ggg	gtg	cgt	gct	cca	acc	aag	gcc	acg	144
Val	Val	Ile	Val	Ser	Arg	His	Gly	Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr	
			35				40					45				

caa	ctg	atg	cag	gat	gtc	acc	cca	gac	gca	tgg	cca	acc	tgg	ccg	gta	192
Gln	Leu	Met	Gln	Asp	Val	Thr	Pro	Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val	
		50				55					60					

aaa	ctg	ggg	gag	ctg	aca	ccg	cgc	ggg	ggg	gag	cta	atc	gcc	tat	ctc	240
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## 10306703.txt

Lys 65	Leu	Gly	Glu	Leu	Thr 70	Pro	Arg	Gly	Gly	Glu 75	Leu	Ile	Ala	Tyr	Leu 80	
gga Gly	cat His	tac Tyr	tgg Trp	cgt Arg 85	cag Gln	cgt Arg	ctg Leu	gta Val	gcc Ala 90	gac Asp	gga Gly	ttg Leu	ctg Leu	cct Pro 95	aaa Lys	288
tgt Cys	ggc Gly	tgc Cys	ccg Pro 100	cag Gln	tct Ser	ggt Gly	cag Gln	gtc Val 105	gcg Ala	att Ile	att Ile	gct Ala 110	gat Asp	gtc Val	gac Asp	336
gag Glu	cgt Arg	acc Thr 115	cgt Arg	aaa Lys	aca Thr	ggc Gly	gaa Glu 120	gcc Ala	ttc Phe	gcc Ala	gcc Ala	ggg Gly 125	ctg Leu	gca Ala	cct Pro	384
gac Asp 130	tgt Cys	gca Ala	ata Ile	acc Thr	gta Val	cat His 135	acc Thr	cag Gln	gca Ala	gat Asp	acg Thr 140	tcc Ser	agt Ser	ccc Pro	gat Asp	432
ccg Pro 145	tta Leu	ttt Phe	aat Asn	cct Pro	cta Leu 150	aaa Lys	act Thr	ggc Gly	gtt Val	tgc Cys 155	caa Gln	ctg Leu	gat Asp	aac Asn	gcg Ala 160	480
aac Asn	gtg Val	act Thr	gac Asp	gcg Ala 165	atc Ile	ctc Leu	gag Glu	agg Arg	gca Ala 170	gga Gly	ggg Gly	tca Ser	att Ile	gct Ala 175	gac Asp	528
ttt Phe	acc Thr	ggg Gly	cat His 180	tat Tyr	caa Gln	acg Thr	gcg Ala	ttt Phe 185	cgc Arg	gaa Glu	ctg Leu	gaa Glu	cgg Arg 190	gtg Val	ctt Leu	576
aat Asn	ttt Phe	ccg Pro 195	caa Gln	tca Ser	aac Asn	ttg Leu	tgc Cys 200	ctt Leu	aaa Lys	cgt Arg	gag Glu	aaa Lys 205	cag Gln	gac Asp	gaa Glu	624
agc Ser 210	tgt Cys	tca Ser	tta Leu	acg Thr	cag Gln	gca Ala 215	tta Leu	cca Pro	tcg Ser	gaa Glu	ctc Leu 220	aag Lys	gtg Val	agc Ser	gcc Ala	672
gac Asp 225	tgt Cys	gtc Val	tca Ser	tta Leu	acc Thr 230	ggt Gly	gcg Ala	gta Val	agc Ser	ctc Leu 235	gca Ala	tca Ser	atg Met	ctg Leu	acg Thr 240	720
gag Glu	ata Ile	ttt Phe	ctc Leu	ctg Leu 245	caa Gln	caa Gln	gca Ala	cag Gln	gga Gly 250	atg Met	ccg Pro	gag Glu	ccg Pro	ggg Gly 255	tgg Trp	768
gga Gly	agg Arg	atc Ile	acc Thr 260	gat Asp	tca Ser	cac His	cag Gln	tgg Trp 265	aac Asn	acc Thr	ttg Leu	cta Leu	agt Ser 270	ttg Leu	cat His	816
aac Asn	gcg Ala	caa Gln 275	ttt Phe	gat Asp	ttg Leu	cta Leu	caa Gln 280	cgc Arg	acg Thr	cca Pro	gag Glu	gtt Val 285	gcc Ala	cgc Arg	agc Ser	864
cgc Arg 290	gcc Ala	acc Thr	ccg Pro	tta Leu	tta Leu	gat Asp 295	ttg Leu	atc Ile	aag Lys	aca Thr	gcg Ala 300	ttg Leu	acg Thr	ccc Pro	cat His	912
cca Pro 305	ccg Pro	caa Gln	aaa Lys	cag Gln	gcg Ala 310	tat Tyr	ggt Gly	gtg Val	aca Thr	tta Leu 315	ccc Pro	act Thr	tca Ser	gtg Val	ctg Leu 320	960

## 10306703.txt

ttt atc gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg	1008
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu	
	325 330 335
gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt	1056
Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly	
	340 345 350
ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag	1104
Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln	
	355 360 365
tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat	1152
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp	
	370 375 380
aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc	1200
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr	
	385 390 395 400
ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca	1248
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala	
	405 410 415
ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg	1296
Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu	
	420 425 430
agatctcatc ta	1308

&lt;210&gt; 10

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; modified phytase enzyme

&lt;400&gt; 10

Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr	
1 5 10 15	
Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser	
20 25 30	
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr	
35 40 45	
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val	
50 55 60	
Lys Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu	
65 70 75 80	
Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys	
85 90 95	
Cys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp	
100 105 110	
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro	
115 120 125	
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp	
130 135 140	
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala	
145 150 155 160	
Asn Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp	
165 170 175	
Phe Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu	
180 185 190	

## 10306703.txt

Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu
		195					200					205			
Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala
	210					215					220				
Asp	Cys	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr
225					230					235					240
Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp
			245						250					255	
Gly	Arg	Ile	Thr	Asp	Ser	His	Gln	Trp	Asn	Thr	Leu	Leu	Ser	Leu	His
			260					265					270		
Asn	Ala	Gln	Phe	Asp	Leu	Leu	Gln	Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser
		275					280					285			
Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu	Ile	Lys	Thr	Ala	Leu	Thr	Pro	His
	290					295					300				
Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly	Val	Thr	Leu	Pro	Thr	Ser	Val	Leu
305					310					315					320
Phe	Ile	Ala	Gly	His	Asp	Thr	Asn	Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu
				325					330					335	
Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly	Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly
			340					345					350		
Gly	Glu	Leu	Val	Phe	Glu	Arg	Trp	Arg	Arg	Leu	Ser	Asp	Asn	Ser	Gln
		355					360					365			
Trp	Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	Arg	Asp
	370					375					380				
Lys	Thr	Pro	Leu	Ser	Leu	Asn	Thr	Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr
385					390					395					400
Leu	Ala	Gly	Cys	Glu	Glu	Arg	Asn	Ala	Gln	Gly	Met	Cys	Ser	Leu	Ala
			405						410					415	
Gly	Phe	Thr	Gln	Ile	Val	Asn	Glu	Ala	Arg	Ile	Pro	Ala	Cys	Ser	Leu
			420					425					430		